Date: Supt. 20, 2001

Respectfully submitted,

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5

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification

Paragraph beginning at page 1 after the title has been amended as follows:

Cross Reference to Related Application

This application claims benefit of U.S. Provisional Application Serial No. 60/243,913, filed October 27, 2000, which application is incorporated herein by reference.

Paragraph beginning at line 21, page 6, has been amended as follows:

Figure 7 shows an amino acid sequence of recombinant human TPO (SEQ ID NO:13).

Paragraph beginning at line 17, page 19, has been amended as follows:

An immunodominant epitope of human thrombopoietin includes amino acids 318 to 332 and has the following sequence (represented in single letter code):

LNTSYTHSQNLSEQ (SEQ ID NO:1)

Paragraph beginning at line 7, page 22, has been amended as follows:

Analysis of the amino acid sequence of human thrombopoietin resulted in the identification of a predicted immunodominant epitope using the service provided by Epivax, Inc. Fourteen out of 15 amino acid residues of the immunodominant peptide identified using antibodies from naïve patients showed 100% homology with the 14 residues at the C-terminal of the 20 amino acid region predicted by EpiVax. The sequence of the predicted immunodominant epitope has an amino acid sequence identical to amino acid residues 312 to 331:

TPTSPLLNTSYTHSQNLSQE (SEQ ID NO: 2)

Paragraph beginning at line 8, page 40, has been amended as follows:

A specific example of a modified polypeptide is a modified thrombopoietin having reduced immunogenicity while retaining substantial therapeutic activity. An

immunodominant epitope in native sequence human thrombopoietin is a c-terminal peptide including amino acids 318 to 332 :

LNTSYTHSQNLSQEG (SEQ ID NO.: 1)

The table beginning at line 14, page 50, with the following rewritten paragraph:

Table 2

Synthetic TPO c-terminal epitope peptides

and corresponding rabbit anti-peptide antibodies

antibody ID#
24
48
28
19
17
49
16
51
15

The peptides have the following sequences:

154- 170	RAPPTTAVPSRTSLVLT (SEQ ID NO: 3)
175-190	PNRTSGLLETNFTASA (SEQ ID NO: 4)
195-211	SGLLKWQQGFRAKIPGL (SEQ ID NO: 5)
218-234	SLDQIPGYLNRIHELLN (SEQ ID NO: 6)
244-259	SRRTLGAPDISSGTSD (SEQ ID NO: 7)
258-268	SDTGSLPPNLQ (SEQ ID NO: 8)

268-283	QPGYSPSPTHPPTGQY (SEQ ID NO: 9)
296-311	VVQLHPLLPDPSAPTP (SEQ ID NO: 10)
318-332	LNTSYTHSQNLSQEG (SEQ ID NO: 1)

Paragraph beginning at line 12, page 52, has been amended as follows:

The entire linear amino acid sequence of human recombinant TPO was provided to EpiVax, Inc. for analysis and prediction of immunodominant epitopes. The results from EpiVax, Inc. identified 3 regions within the c-terminal epitope that have class II MHC binding motifs. One of these predicted epitope regions (identical to amino acids 312-331) is shown:

TPTSPLLNTSYTHSQNLSQE (SEQ ID NO: 2)

Paragraph beginning at line 17, page 53, has been amended as follows:

A cDNA corresponding to the hTPO entire open reading frame was obtained by PCR using the oligonucleotide primes of the following Table.

CHO Expression Vector PCR Prim	ssion Vector PCR Primers
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Cla.FL.F2 5' ATC GAT ATC GAT AGC CAG ACA CCC CGG CCA G 3'
(SEQ ID NO:11)
ORF.Sal 5' AGT CGA CGT CGG CAG TGT CTG AGA ACC 3'
(SEQ ID NO:12)

PRK5-hmpl I was used as template for the reaction in the presence of pfu DNA polymerase (Stratagene). Initial denaturation was for 7 min. at 94°C followed by 25 cycles of amplification (1 min. at 94°C, 1 min. at 55°C and 1 min. at 72°C). Final extension was for 15 min. at 72°C. The PCR product was purified and cloned between the restriction sites Clal and Sall of the plasmid pSV15.ID.LL to obtain the vector pSV15.ID.LL.MLORF.The sequence of the construct was verified.